REMARKS

Amendments to the claims have been made in response the Examiner's comments and concerns and were not made previously for that reason.

No new matter enters the claims or specification by any of these amendments, and Applicants believe that these amendments do not raise new issues.

Please cancel claims 19-24.

Please amend claims 1, 2, and 17 as indicated above.

Please add new claims 25-28 as indicated above.

The Pending Claims

Prior to the entry of these Amendments, Claims 1, 2, and 17 are pending.

The Office Action

Claim 1 is rejected under 35 U.S.C §112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was file, had possession of the claimed invention.

Claim 1-2 and 17 are rejected under 35 U.S.C §112, first paragraph, because the specification, does not reasonably provide enablement for other isolated polynucleotides, or for transgenic plants comprising other polynucleotides or exhibiting phenotypic characteristics as a consequence of altered levels of expression or other polynucleotides.

Claim 1 is rejected under 35 U.S.C §112, second paragraph as being indefinite for the recitation of "the complement thereof", and because "increases is a relative term lacking a comparative basis.

Claims 1-2 and 17 are rejected under 35 U.S.C §102(b) as being anticipated by Zhang et al. because the claimed invention is not limited to polynucleotides that are fully complementary to the nucleotide sequences of SEQ ID NO: 1 or encoding SEQ ID NO: 2.

Amendments

Applicants have canceled Claims 19-24. New Claims 25-27, which are derived from Claim 1 and are directed to polynucleotide sequence that hybridize under stringent conditions

with SEQ ID NO: 1 or nucleotide sequences encoding a polypeptide comprising SEQ ID NO: 2, have been added.

Support

Support for the amendment to Claim 1 is provided by Claim 1 as filed, and on page 36, lines 14-19 of the specification (control plants transformed with an empty transformation vector).

Support for the amendment to Claim 2 is provided by Claim 2 as filed.

Support for new Claims 25-27 is provided by Claims 1 and 2 as filed, as well as the specification on page 11, lines 15-23.

Support for new Claim 28 is provided by, for example, Claim 1 as filed, and in the specification on page 6, lines 16-23 (expression cassettes or vectors, and inducible or constitute regulatory sequences) page 11, lines 15-23 (defined conditions of stringency), on page 34, line 13 through page 36, line 30 (method for producing a plant having increased biomass by overexpressing G1073) and on page 36, lines 14-19 (control plants transformed with an empty transformation vector).

Response to Rejections

Elections/Restrictions

New submitted Claims 19-24 have been withdrawn because the Examiner believed that these claims were directed to inventions that were not previously restricted but not elected.

Applicants have added new Claims 25-27, which are derived from Claim 1(e) and Claim 2 as filed. Claims 25-27 have been separated from Claim 1 for reasons of form and readability. These claims are directed to polynucleotide sequence that hybridize under stringent conditions with SEQ ID NO: 1 or nucleotide sequences encoding a polypeptide comprising SEQ ID NO: 2. New Claim 28 is directed to a process for making the compositions of Claim 1.

Applicants believe that the process of Claim 28 and the transgenic plant of Claim 1 do not warrant further restriction in that:

Claims 1, 25 and 28 are directed to the same nucleotide sequences;

the process of Claim 28 produces the products (the transgenic plants) of Claims 1 and 25 and does not produce another product; and

the transgenic plant of Claims 1 and 25, which comprises a recombinant polynucleotide, cannot be made by another process, since transgenic plants (and ultimately their progeny), regardless of whether the transformation is mediated by agrobacteria, microinjection,

electroporation, biolistics, etc., are created by transformation with a vector or cassette comprising a nucleotide sequence (and, typically, regulatory sequences; see page 6, lines 16-23 of the specification).

Furthermore, stable transformation of plant cells or the establishment of transgenic plants is achieved with expression vectors (see p. 17, lines 13-20 of the specification).

Accordingly, Applicants believe that the presently amended and presented claims should be considered without further restriction or be subject to withdrawal on the basis that they disclose patentably distinct inventions.

Claim Rejections - 35 USC § 112, first paragraph

This rejection has been avoided by the amendments to the claims.

The claims, as amended, are no longer directed to conservatively substituted polypeptide variants, or silently substituted nucleotide sequences.

The claims, as amended, are no longer directed to altered levels of expression of other polynucleotides

The claims, as amended, are no longer directed to conserved regions.

The claims, as amended, are no longer directed to sequences with a particular percent identity to the presently disclosed sequences

Claims 25 and 26 are directed to nucleotides that hybridize with a nucleotide sequence comprising SEQ ID NO: 1 or encoding a polypeptide comprising SEQ ID NO: 2, under stringent conditions that comprise wash conditions of 0.2 x SSC to 2.0 x SSC, 0.1% SDS at 60-65° C.

Applicants note that the USPTO has stated that "6XSSC and 65 degrees Celsius" constitute "highly stringent hybridization conditions", that "a person of skill in the art would not expect substantial variation among species encompassed within the scope of the claims because the highly stringent conditions set forth in the claim yield structurally similar DNAs. Thus, a representative number of species is disclosed, since highly stringent hybridization conditions in combination with the coding function of DNA and the level of skill and knowledge in the art are adequate to determine that applicant was in possession of the claimed invention "Revised Interim Written Description Guidelines Training Materials", www.uspto.gov/web/offices/pac/writtendesc.pdf" (the relevant pages are attached). One of skill in knowledge in the art would also know that hybridization wash conditions of 0.2 x SSC to 2.0 x SSC, 0.1% SDS at 60-65° C, constitute stringent conditions (SDS is included in the washing buffer to decrease non-specific binding, and has significantly less of an effect on stringency than salt concentration or temperature). At 65° C,

the wash conditions specified in the claims, 0.2 x SSC to 2.0 x SSC, 0.1% SDS, are obviously even more stringent than 6X SSC and at the same temperature.

Regarding wash conditions at lower temperatures, Figure 1 shows a graph of the theoretical melting temperatures vs. xSSC for a nucleic acid molecule with 53.9% G+C content, as found in G1073 (SEQ ID NO: 1), is shown. The calculated data were derived using the program Oligo, version 5 (Molecular Biology Insights, Inc., Cascade, CO), for a chain length of 75 bases, and the calculations are based on the formula of Meinkoth and Wahl (1984) *Anal. Biochem.* 138: 267-284:

$T_m = 81.5°\ C + 16.6\ (\log M) + 0.41\ (\%\ GC) - 0.61\ (\%\ formamide) - 500/L$

T_m = melting temperature;

M =

% formamide = 0

L= sequence length

For sequences longer than 75 bases, the Meinkoth-Wahl formula becomes less valuable in predicting actual melting temperatures, which increase slightly but not to the extent predicted by the formula. In any event, the differences between the calculated melting temperatures at each SSC concentration and a given experimental temperature used (e.g., 60° C to 65° C) remain constant because the equation term (-500/L) is independent of temperature and SSC concentration.

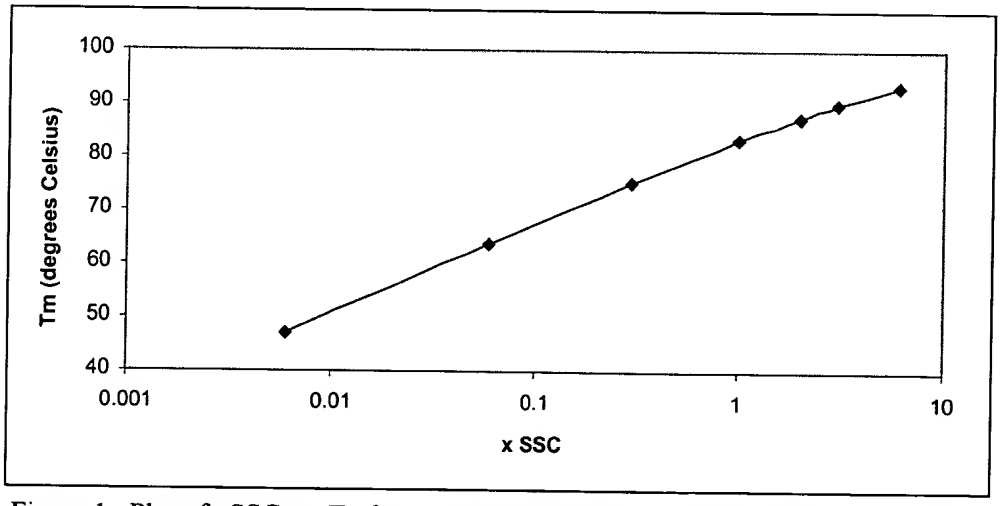

Figure 1. Plot of xSSC vs. T_m for a nucleic acid molecule with 53.9% G+C content

Thus, at 6X SSC, the melting temperature of a nucleic acid molecule 75 bases long with a 53.9% G+C content is calculated to be about 93° C, or about 28° C above the 65° C used in the experimental conditions defined by the USPTO in the above cited "Training Materials". A significantly longer molecule would have a slightly greater melting temperature, for example, 95° C, in which case the difference would be about 29° C above the 65° C used in the experimental conditions defined by the USPTO.

At 2X SSC, the melting temperature of the same nucleic acid molecule is calculated to be about 88° C, or about 28° C above the low end of the range (60° C) used in the experimental conditions to which the claims are directed. A significantly longer molecule would have a slightly greater melting temperature, for example, 89° C, in which case the difference would be about 29° C above the 60° C low end of the range found in the claims, the same difference as with 6X SSC.

At 0.2X SSC, the melting temperature of the 75 base nucleic acid molecule is calculated to be about 70° C, or only about 10° C above the low end of the range (60° C) used in the experimental conditions to which the claims are directed. One of skill in the art would understand that wash conditions that decrease the difference between the experimental temperature and the theoretical melting temperature at a particular ionic strength provide greater stringency, in this case than the conditions used in the USPTO example.

One of skill in the art would know that the stringency of the hybridization can be accommodated in either the hybridization or wash steps, and stringency is determined by the more stringent of either step; i.e., the stringency of a hybridization procedure will be no less than the stringency of the wash conditions. In fact, hybridization specificity is typically determined by post-hybridization washes, with the critical factors being the ionic strength and temperature of the final wash solution. Thus the range of conditions specified in the amended claims are calculated to be at least as stringent (2X SSC, and 60° C) or more stringent (<2X SSC, and 60° C) as the 6X SSC and 65° C, taught in the above cited "Training Materials", the latter conditions being described as "adequate to determine that applicant was in possession of the claimed invention".

Accordingly, Applicants respectfully request that the rejections under 35 USC § 112, first paragraph, be withdrawn.

Claim Rejections - 35 USC § 112, second paragraph

This rejection of the claims is avoided by the amendment to the claims.

The Examiner has expressed concern that phrase "or complement thereof" is unclear with regard to what it refers. Claim 1 has been amended to address this concern; Applicants believe

that the amendment to "-- a sequence that is ***fully*** complementary to the nucleotide sequence encoding a polypeptide comprising SEQ ID NO: 2 --, and -- a sequence that is ***fully*** complementary to the nucleotide sequence comprising SEQ ID NO: 1 --, follows the Examiner's suggestion (***emphasis*** added).

Regarding the recitation of "increases", this part of the indefiniteness rejection has been avoided by the amendment of Claim 1 to " increases a plant's biomass -- as compared to a control plant not transformed with said recombinant polynucleotide-- " .

Accordingly, Applicants respectfully request that the rejections under 35 USC § 112, second paragraph, be withdrawn.

Claim Rejections - 35 U.S.C. § 102(b)

The Examiner has rejected Claims 1, 2 and 17 as being anticipated by Zhang et al. because the claimed invention is, in the Examiner's words, not limited to polynucleotides that are fully complementary to a nucleotide sequence of SEQ ID NO: 1 or encoding SEQ ID NO: 2, as complement encompasses a single nucleotide base.

Applicants disagree with the opinion that "it is unclear what type of complementary nucleotide sequence" Applicant intends to claim" (Paper 11). First, with respect to polynucleotide sequences, a "complementary sequence" has clear meaning in the art. See the USPTO's "Synopsis of Application of Written Description Guidelines", Example 9, wherein, given the exemplary claim that includes "[a]n isolated nucleic acid that specifically hybridizes ... to the complement of the sequence set forth in SEQ ID NO: 1", "a person of skill in the art would not expect substantial variation among species encompassed within the scope of the claims because the highly stringent conditions set forth in the claim yield structurally similar DNAs". The analysis provided and directed to 112 USC paragraph 1, written description, would be moot if this example did not distinctly claim a representative number of species. Applicants also believe that the specific functional language within amended Claim 1 further makes the claim definite, as a "sequence" of a single base or a non-functioning subsequence cannot serve to increase a plant's biomass, and thus Claim 1 and its dependent claims cannot be anticipated by Zhang et al.

However, in the interest of advancing the prosecution of this application, Applicants have avoided this rejection of Claims 1, 2 and 17 by the present amendment to the Claim 1.

Accordingly, Applicants respectfully request that the rejections under 35 USC § 102 be withdrawn.

CONCLUSION

In view of the above amendment and remarks, it is submitted that this application is now ready for allowance. Early notice to that effect is solicited. If, in the opinion of the Examiner, a telephone conference would expedite the prosecution of the subject application, the Examiner is invited to call the undersigned at (510) 259-6138.

Applicants believe that no additional fee is due with this communication. However, if the USPTO determines that a fee is due, the Commissioner is hereby authorized to charge Mendel Biotechnology, Inc. Deposit Account No. **501025. This form is enclosed in duplicate.**

Respectfully submitted,
MENDEL BIOTECHNOLOGY, INC.

Date: September 24, 2003

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